

0590
2606
4

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/042,894A

DATE: 06/05/2002

TIME: 09:54:24

Input Set : A:\1286 AMD SEQLIST.TXT

Output Set: N:\CRF3\06052002\J042894A.raw

P.6

ENTERED

4 <110> APPLICANT: Shi, Jinrui
5 Beach, Larry
6 Wang, Hongyu
7 Rafalski, Antoni J.
8 Cahoon, Rebecca E.
10 <120> TITLE OF INVENTION: Novel Inositol Polyphosphate Kinase
11 Genes and Uses Thereof
13 <130> FILE REFERENCE: 1286
15 <140> CURRENT APPLICATION NUMBER: US 10/042,894A
16 <141> CURRENT FILING DATE: 2002-01-09
18 <150> PRIOR APPLICATION NUMBER: US 60/261,465
19 <151> PRIOR FILING DATE: 2001-01-12
21 <160> NUMBER OF SEQ ID NOS: 37
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1169
27 <212> TYPE: DNA
28 <213> ORGANISM: Zea mays
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (84)...(806)
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36 cttgctccca tagtccccat acc atg ccc gac ctc cac ccg ccg gag cac caa 113
37 Met Pro Asp Leu His Pro Pro Glu His Gln
38 1 5 10
40 gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc ccg ctc atc gac 161
41 Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp
42 15 20 25
44 ggc tcc ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt ggg gag 209
45 Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu
46 30 35 40
48 cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg 257
49 His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro
50 45 50 55
52 gcc cgc atc cga gac acc ttc ttc ccc ccg ttc cac ggc acg cga ctc 305
53 Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu
54 60 65 70
56 ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc 353
57 Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu
58 75 80 85 90
60 gac gag ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag 401
61 Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys

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62	95	100	105	
64	atc ggc gcc atc acg tgg cca ccg agt tcg ccg gag ccc tac atc gcc			449
65	Ile Gly Ala Ile Thr Trp Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala			
66	110	115	120	
68	aag tac ctc gcc aag gac cgc ggg acc acg agc gtt ctg ctc gga ttc			497
69	Lys Tyr Leu Ala Lys Asp Arg Gly Thr Thr Ser Val Leu Leu Gly Phe			
70	125	130	135	
72	cgc gtc ttg cgt ccg agt cgt cgg ccc cga ggg cgc cgt gtg gcg gac			545
73	Arg Val Leu Arg Pro Ser Arg Arg Pro Arg Gly Arg Arg Val Ala Asp			
74	140	145	150	
76	gga gcg ccc gga ggt gaa ggc tat gga cac cgt cgg cgt ccg ccg cgt			593
77	Gly Ala Pro Gly Gly Glu Gly Tyr Gly His Arg Arg Arg Pro Pro Arg			
78	155	160	165	170
80	gct ccg gcg cta cgt gtc atc cgc ttg ccg acg agg gga tgg act gcg			641
81	Ala Pro Ala Leu Arg Val Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala			
82	175	180	185	
84	cgc tcg cgg cgg cgg tgt acg gag gaa aag gtg gag tct tgt cac agc			689
85	Arg Ser Arg Arg Cys Thr Glu Glu Lys Val Glu Ser Cys His Ser			
86	190	195	200	
88	tgc gcg agc tca agg cat ggt tgg agg agc aga ctc tgt tcc act tct			737
89	Cys Ala Ser Ser Arg His Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser			
90	205	210	215	
92	act cgg cgt cga ttc ttc tgg gct atg atg ctg ctg cag tcg cag cag			785
93	Thr Arg Arg Arg Phe Phe Trp Ala Met Met Leu Leu Gln Ser Gln Gln			
94	220	225	230	
96	gcg gag gtg ggg gtg ggg taa cagtgaagct ggtggactt gccatgtgg			836
97	Ala Glu Val Gly Val Gly *			
98	235	240		
100	ccgagggtga tgggtgatt gaccacaact tcctggcga gctctgttag ctgatcaagt			896
101	tcgttctga cattgttcca gagactcctt agacgcagcc tttgggtcct tcttaagaga			956
102	ggatcctgac attttgatt tgataacaaa ggaagcactt tcagctgcaa aaaaagaaaag			1016
103	cagcagttag gatgaagatg acagtagtga ggaaagttcg gatgatgagc caacaaaagt			1076
104	tgaagaaaag aaggctccaa aagtatcaga aaacatttggaa tctgaggatg aatcttctga			1136
105	agacgagagt gataaagaca gtgaagagcc tca			1169
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108	<211> LENGTH: 240			
109	<212> TYPE: PRT			
110	<213> ORGANISM: Zea mays			
112	<400> SEQUENCE: 2			
113	Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala			
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115	Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr			
116	20	25	30	
117	Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr			
118	35	40	45	
119	Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr			
120	50	55	60	
121	Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln			
122	65	70	75	80

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Input Set : A:\1286 AMD SEQLIST.TXT

Output Set: N:\CRF3\06052002\J042894A.raw

123 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
 124 85 90 95
 125 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
 126 100 105 110
 127 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp
 128 115 120 125
 129 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser
 130 130 135 140
 131 Arg Arg Pro Arg Gly Arg Arg Val Ala Asp Gly Ala Pro Gly Gly Glu
 132 145 150 155 160
 133 Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val
 134 165 170 175
 135 Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Arg Cys
 136 180 185 190
 137 Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His
 138 195 200 205
 139 Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe
 140 210 215 220
 141 Trp Ala Met Met Leu Leu Gln Ser Gln Gln Ala Glu Val Gly Val Gly
 142 225 230 235 240
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 146 <211> LENGTH: 923
 147 <212> TYPE: DNA
 148 <213> ORGANISM: Zea mays
 150 <220> FEATURE:
 151 <221> NAME/KEY: CDS
 152 <222> LOCATION: (53)...(736)
 154 <400> SEQUENCE: 3
 155 accgcttcca ccatcgccac tcgtcacccc ttgctccat agtccccata cc atg ccc 58
 156 Met Pro
 157 1
 158 gac ctc cac ccg ccg gag cac caa gtc gcc ggt cac cgc gcc tcc gcc 106
 159 Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
 160 5 10 15
 161 agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg 154
 162 Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
 163 20 25 30
 164 ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202
 165 Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
 166 35 40 45 50
 167 ttc tcc gcc cac gcc gtc ccg gcc cgc atc cga gac acc ttc ttc 250
 168 Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
 169 55 60 65
 170 ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298
 171 Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
 172 70 75 80
 173 gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag 346
 174 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu
 175 85 90 95

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/042,894A

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Input Set : A:\1286 AMD SEQLIST.TXT

Output Set: N:\CRF3\06052002\J042894A.raw

183	gcg	ccc	tgc	gtc	gca	gac	atc	aag	atc	ggc	gcc	atc	acg	tgg	cca	ccg	394
184	Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys	Ile	Gly	Ala	Ile	Thr	Trp	Pro	Pro	
185	100				105				110								442
187	agt	tcg	ccg	gag	ccc	tac	atc	gcc	aag	tgc	ctc	gcc	atg	gac	ccg	ggg	
188	Ser	Ser	Pro	Glu	Pro	Tyr	Ile	Ala	Lys	Cys	Leu	Ala	Met	Asp	Arg	Gly	
189	115				120				125				130				490
191	acc	acc	agc	gtt	ctg	ctc	gga	ttc	ccg	gtc	tcc	ggc	gtc	cga	gtc	gtc	
192	Thr	Thr	Ser	Val	Leu	Leu	Gly	Phe	Arg	Val	Ser	Gly	Val	Arg	Val	Val	
193					135				140				145				538
195	gtc	ccc	gag	ggc	gcc	gtg	tgg	cg	acg	gag	ccg	ccg	gag	gtg	aag	gct	
196	Val	Pro	Glu	Gly	Ala	Val	Trp	Arg	Thr	Glu	Arg	Pro	Glu	Val	Lys	Ala	
197					150				155				160				586
199	atg	gac	acc	gtc	ggc	gtc	ccg	cg	gtg	ctc	ccg	ccg	tac	gtg	tca	tcc	
200	Met	Asp	Thr	Val	Gly	Val	Arg	Val	Leu	Arg	Arg	Arg	Tyr	Val	Ser	Ser	
201	165				170				175								634
203	gct	tgc	cga	cga	ggg	gat	gga	ctg	ccg	gtc	ccg	ggc	gg	gtt	gta	ccg	
204	Ala	Cys	Arg	Arg	Gly	Asp	Gly	Leu	Arg	Ala	Arg	Gly	Gly	Gly	Val	Arg	
205	180				185				190								682
207	agg	aaa	agg	tgg	agt	ctt	gtc	act	gct	ccg	gtc	ccg	caa	ggc	gtg	gtt	
208	Arg	Lys	Arg	Trp	Ser	Leu	Val	Thr	Ala	Ala	Arg	Ala	Gln	Gly	Val	Val	
209	195				200				205				210				730
211	cga	gga	gca	gcc	tct	gtt	cca	ctt	cta	ctc	ggc	gtc	gat	tct	tct	ggg	
212	Arg	Gly	Ala	Ala	Ser	Val	Pro	Leu	Leu	Leu	Gly	Val	Asp	Ser	Ser	Gly	
213					215				220				225				786
215	cta	tga	tgctgctgca	gtcgcagcag	gcggaggtgg	gggtgggtta	acagtgaagc										846
216	Leu	*															906
219	tgg	tgg	actt	tgccatgtg	gccgagggtg	atgggtgtat	tgaccacaac	ttcctggcg									923
220	gct	cgt	ctg	cta	gctgatcaag	ttcgtttctg	acattgttcc	agagactcct	cagacgcagc								
221	ctt	ttt	gggtcc	ttcttaa													
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224	<211>	LENGTH:	227.														
225	<212>	TYPE:	PRT														
226	<213>	ORGANISM:	Zea mays														
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230	1				5				10				15				
231	Ser	Ala	Ser	Lys	Pro	Gly	Pro	Leu	Ile	Asp	Gly	Ser	Gly	Leu	Phe	Tyr	
232					20				25				30				
233	Lys	Pro	Leu	Gln	Ala	Gly	Asp	Arg	Gly	Glu	His	Glu	Val	Ala	Phe	Tyr	
234					35				40				45				
235	Glu	Ala	Phe	Ser	Ala	Ala	His	Ala	Ala	Val	Pro	Ala	Arg	Ile	Arg	Asp	Thr
236					50				55				60				
237	Phe	Phe	Pro	Arg	Phe	His	Gly	Thr	Arg	Leu	Leu	Pro	Thr	Glu	Ala	Gln	
238					65				70				75				80
239	Pro	Gly	Glu	Pro	His	Pro	His	Leu	Val	Leu	Asp	Asp	Leu	Leu	Ala	Gly	
240					85				90				95				
241	Phe	Glu	Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys	Ile	Gly	Ala	Ile	Thr	Trp	
242					100				105				110				
243	Pro	Pro	Ser	Ser	Pro	Glu	Pro	Tyr	Ile	Ala	Lys	Cys	Leu	Ala	Met	Asp	

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244	115	120	125														
245	Arg	Gly	Thr	Thr	Ser	Val	Leu	Leu	Gly	Phe	Arg	Val	Ser	Gly	Val	Arg	
246	130		135		140												
247	Val	Val	Val	Pro	Glu	Gly	Ala	Val	Trp	Arg	Thr	Glu	Arg	Pro	Glu	Val	
248	145		150		155		160										
249	Lys	Ala	Met	Asp	Thr	Val	Gly	Val	Arg	Arg	Val	Leu	Arg	Arg	Tyr	Val	
250			165		170		175										
251	Ser	Ser	Ala	Cys	Arg	Arg	Gly	Asp	Gly	Leu	Arg	Ala	Arg	Gly	Gly		
252			180		185		190										
253	Val	Arg	Arg	Lys	Arg	Trp	Ser	Leu	Val	Thr	Ala	Ala	Arg	Ala	Gln	Gly	
254			195		200		205										
255	Val	Val	Arg	Gly	Ala	Ala	Ser	Val	Pro	Leu	Leu	Leu	Gly	Val	Asp	Ser	
256			210		215		220										
257	Ser	Gly	Leu														
258	225																
261	<210>	SEQ	ID	NO:	5												
262	<211>	LENGTH:	923														
263	<212>	TYPE:	DNA														
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272										Met	Pro						
273										1							
275	gac	ctc	cac	ccg	ccg	gag	cac	caa	gtc	gcc	ggt	cac	cgc	gcc	tcc	gcc	106
276	Asp	Leu	His	Pro	Pro	Glu	His	Gln	Val	Ala	Gly	His	Arg	Ala	Ser	Ala	
277									5	10	15						
279	agc	aag	ccg	ggc	ccg	ctc	atc	gac	ggc	tcc	ggc	ctc	tcc	tac	aag	ccg	154
280	Ser	Lys	Pro	Gly	Pro	Leu	Ile	Asp	Gly	Ser	Gly	Leu	Phe	Tyr	Lys	Pro	
281									20	25	30						
283	ctc	cag	gcc	ggc	gac	cgt	ggg	gag	cac	gag	gtc	gct	ttc	tat	gag	gcg	202
284	Leu	Gln	Ala	Gly	Asp	Arg	Gly	Glu	His	Glu	Val	Ala	Phe	Tyr	Glu	Ala	
285									35	40	45					50	
287	ttc	tcc	gcc	cac	gcc	gtc	ccg	gcc	cgc	atc	cga	gac	acc	ttc	ttc		250
288	Phe	Ser	Ala	His	Ala	Ala	Val	Pro	Ala	Arg	Ile	Arg	Asp	Thr	Phe	Phe	
289									55	60	65						
291	ccc	cgg	ttc	cac	ggc	acg	cga	ctc	ctc	ccc	acc	gag	gcg	cag	ccc	ggg	298
292	Pro	Arg	Phe	His	Gly	Thr	Arg	Leu	Leu	Pro	Thr	Glu	Ala	Gln	Pro	Gly	
293									70	75	80						
295	gag	ccg	cat	ccg	cac	ctc	gtc	ctc	gac	gac	ctc	ctc	gcg	gga	ttt	gag	346
296	Glu	Pro	His	Pro	His	Leu	Val	Leu	Asp	Asp	Leu	Leu	Ala	Gly	Phe	Glu	
297									85	90	95						
299	gcg	ccc	tgc	gtc	gca	gac	atc	aag	atc	ggc	gcc	atc	acg	tgg	cca	ccg	394
300	Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys	Ile	Gly	Ala	Ile	Thr	Trp	Pro	Pro	
301									100	105	110						
303	agt	tgc	ccg	gag	ccc	tac	atc	gcc	aag	tgc	ctc	gcc	atg	gac	cgc	ggg	442
304	Ser	Ser	Pro	Glu	Pro	Tyr	Ile	Ala	Lys	Cys	Leu	Ala	Met	Asp	Arg	Gly	

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/042,894A

DATE: 06/05/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 12,283,481,491,598,617,619,626,637
Seq#:18; N Pos. 9,15,47,135,230,335,359,403,415,419,450,480,507,509,518
Seq#:19; N Pos. 85,226,277,294,317,331,351
Seq#:30; Xaa Pos. 3,12,14,15,18,25,27
Seq#:31; Xaa Pos. 3,12,14,15,18,25,27
Seq#:32; Xaa Pos. 3,12,14,15,18,25,27
Seq#:33; Xaa Pos. 3,12,14,15,18,25,27
Seq#:34; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:35; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:36; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:37; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38